

query 111734-112069  
of Seq ID #1

ORF 1089

CHTTRTUFB  
LOCUS CHTTRTUFB 1414 bp DNA linear BCT 16-FEB-1995  
DEFINITION Chlamydia trachomatis elongation factor Tu (TufB) gene, complete  
cds.  
ACCESSION M74221  
VERSION M74221.1 GI:666129  
KEYWORDS elongation factor Tu.  
SOURCE Chlamydia trachomatis  
ORGANISM Chlamydia trachomatis  
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
REFERENCE 1 (bases 1 to 1414)  
AUTHORS Cousineau,B., Cerpa,C., Lefebvre,J. and Cedergren,R.  
TITLE The sequence of the gene encoding elongation factor Tu from  
Chlamydia trachomatis compared with those of other organisms  
JOURNAL Gene 120 (1), 33-41 (1992)  
MEDLINE 93013017  
PUBMED 1398121  
REFERENCE 2 (bases 1 to 1414)  
AUTHORS Cousineau,B.  
TITLE Direct Submission  
JOURNAL Submitted (19-OCT-1991) Benoit Cousineau, Biochimie, University of  
Montreal, Montreal, Quebec, Canada, H3C 3J7  
COMMENT On Feb 16, 1995 this sequence version replaced gi:144630.  
Original source text: Chlamydia trachomatis DNA.  
FEATURES  
Location/Qualifiers  
source 1. .1414  
/organism="Chlamydia trachomatis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:813"  
gene 118. .1302  
/gene="TufB"  
CDS 118. .1302  
/gene="TufB"  
/codon\_start=1  
/transl\_table=11  
/product="elongation factor Tu"  
/protein\_id="AAA62238.1"  
/db\_xref="GI:666130"  
/translation="MSKETFQRNKPINIGAIGHVDHGRTTLTAAITRTLSGDGLADF  
RDYSSIDNTPEEKARGIPINASHVEYETANRHYAHVDCPCHADYVKNMITGAAQMDGA  
ILVVSATDGAMPQTKEHILLARQVGVPYIVVFLNKIDMISEEDAELVDLVEMELAELL  
EEKGYKGCPIIRGSALKALEGDAAYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV  
FSISGRGTVVVTGRIERGIVKVSQVQLVGLRDTKETLLLGLEMFRKNSQKVRAGENVG  
LLLRGIGKNDVERGMVCLPNSVKPHTRFKCAVYVLQKEEGGRHKPFPTGYRPQFFFL  
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IA"

#### ORIGIN

Query Match 96.1%; Score 323; DB 1; Length 1414;  
Best Local Similarity 99.1%; Pred. No. 1.5e-79;  
Matches 336; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 CATCGTTGTTTTTCTCAATAAAATTGACATGATTTCCGAAGAAGACGCTGAATTGGTCTGA 60  
|  
Db 507 CATCGTTGTTTTTCTCAATAAAATTGACATGATTTCCGAAGAAGACGCTGAATTGGTCTGA 566

Qy	61	CTTGGTTGAGATGGAGTTGGCTGAGCTTCTTGAAGAGAAAGGATACAAAGGGTGTCCAAT	120
Db	567	CTTGGTTGAGATGGAGTTGGCTGAGCTTCTTGAAGAGAAAGGATACAAAGGGTGTCCAAT	626
Qy	121	CATCAGAGGTTCTGCTCTGAAAGCTTTGGAAGGGGATGCTGCATACATAGAGAAAGTTCG	180
Db	627	CATCAGAGGTTCTGCTCTGAAAGCTTTGGAAGGGGATGCTGCATACATAGAGAAAGTTCG	686
Qy	181	AGAGCTAATGCAAGCCGTCGATGATAATATCCCTACTCCAGAAAGAGAAATTGACAAGCC	240
Db	687	AGAGCTAATGCAAGCCGTCGATGATAATATCCCTACTCCAGAAAGAGAAATTGACAAGCC	746
Qy	241	TTTCTTAATGCCCATTTGAGGACGTGTTCTCTATCTCCGGACGAGGAAC---AGTAACTGG	297
Db	747	TTTCTTAATGCCCATTTGAGGACGTGTTCTCTATCTCCGGACGAGGAAGTGTAGTAACTGG	806
Qy	298	ACGTATTGAGCGTGGAATTGTTAAAGTTTCCGATAAAGT	336
Db	807	ACGTATTGAGCGTGGAATTGTTAAAGTTTCCGATAAAGT	845

query 467981-468262  
of Seq 10 #1

ORF 1140

US-08-896-346-1/c  
; Sequence 1, Application US/08896346  
; Patent No. 6207647  
; GENERAL INFORMATION:  
; APPLICANT: Black, Michael T.  
; TITLE OF INVENTION: No. 6207647el RatA  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/896,346  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: GM10040  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1476 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-896-346-1

Query Match 100.0%; Score 282; DB 3; Length 1476;  
Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACAGGTACCGCATGTTTCAAAACACTGAGATCTACATCAATAATGCGACTGCCTTCACGT	60
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Qy	61	TCCATAACAGCAAGAGCTTCGAAAAAGTTTTCTTTACAATCTTCTTGCAAGTCCGTCTAGG	120
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Qy	121	AATCCTCTAGGAACTCCGATTAACTTAGGAACTTCCAATGACAAGGCTTGCGAAAACGTC	180
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Qy 181 CCTTTAAAAAAGTCTCTCGTAGTGGAATCTTTGGGATCACGACCAGCAAAGGCATCCATT 240  
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Db 731 CCTTTAAAAAAGTCTCTCGTAGTGGAATCTTTGGGATCACGACCAGCAAAGGCATCCATT 672  
  
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